ID NO:18) (**Fig. 6a**) and of the BIR domains from DIAP1-BIR2 (SEQ ID NO: 30), DIAP-BIR1 (SEQ ID NO:19), XIAP-BIR3 (SEQ ID NO:20), XIAP-BIR2 (SEQ ID NO:21), XIAP-BIR1 (SEQ ID NO:22), and survivin (SEQ ID NO:23) (**Fig. 6b**). The zinc-chelating residues are shown in red whereas the conserved amino acids are highlighted in yellow. Red and yellow arrows identify those residues that make intermolecular hydrogen bonds using their side chain and main chain atoms, respectively. The solvent accessibility for the peptides (Fig. 10a) and the secondary structural elements for the DIAP1-BIR2 domain (Fig. 10b) are indicated below the sequence alignment.--

3. At page 10, please replace the paragraph appearing at lines 12-19 with the following amended paragraph.

--**Fig. 13.** Effect of *Drosophila* pentapeptides, Hid-5, Reaper-5, and Grim-5 on XIAP inhibition on caspase-3 activation. **Fig. 13a,** The amino acid sequences of Smac-5 (SEQ ID NO:24) and the NH_2-terminal sequence of Hid (SEQ ID NO:26), Reaper (SEQ ID NO:27) and Grim (SEQ ID NO:28) are shown. The conserved pentapeptide sequences are boxed. **Fig. 13b,** 10-1000 μM of pentapeptides as indicated were assayed in a reaction containing recombinant human Apaf-1 and procaspase-9, XIAP, purified cytochrome c, and in vitro translated ^{35}S-labeled procaspase-3. The procaspase-3 cleavage activity was measured by phosphorimaging.--